

<!--StartFragment-->GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2007, 16:27:56 ; Search time 3229 Seconds
 (without alignments)
 18793.786 Million cell updates/sec

Title: US-10-524-193A-110
 Perfect score: 8189
 Sequence: 1 gagctcgaccgcgcgggtcc.....aacggccaactctcgttcaa 8189

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_200701:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*
 16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	IDB	ID	Description
1	8189	100.0	8189	12	ADL06264	Adl06264 DNA seque
2	8189	100.0	8189	13	ADU38632	Adu38632 TipA prom
3	8154.6	99.6	8207	13	ADU38670	Adu38670 TipA prom
4	8127.8	99.3	8211	13	ADU38671	Adu38671 TipA prom
5	8118.6	99.1	8166	12	ADL06260	Adl06260 DNA seque
6	8118.6	99.1	8166	13	ADT49718	Adt49718 Cell-free
7	8118.6	99.1	8166	13	ADU38628	Adu38628 TipA prom
8	8105	99.0	8184	12	ADL06267	Adl06267 DNA seque
9	8105	99.0	8184	13	ADU38635	Adu38635 TipA prom
10	8103.8	99.0	8169	12	ADL06261	Adl06261 DNA seque

	11	8103.8	99.0	8169	13	ADU38629	Adu38629	TipA	prom
	12	8103	98.9	8183	12	ADL06265	Adl06265	DNA	seque
	13	8103	98.9	8183	13	ADU38633	Adu38633	TipA	prom
	14	8039.4	98.2	8160	12	ADL06263	Adl06263	DNA	seque
	15	8039.4	98.2	8160	13	ADU38631	Adu38631	TipA	prom
	16	8036.2	98.1	8160	12	ADL06262	Adl06262	DNA	seque
	17	8036.2	98.1	8160	13	ADT49716	Adt49716	Cell-free	
	18	8036.2	98.1	8160	13	ADU38630	Adu38630	TipA	prom
	19	7973	97.4	8123	12	ADL06266	Adl06266	DNA	seque
	20	7973	97.4	8123	13	ADU38634	Adu38634	TipA	prom
	21	7264	88.7	8994	13	ADT49715	Adt49715	Cell-free	
	22	7206.4	88.0	8971	12	ADL71919	Adl71919	Nucleotid	
	23	6332.8	77.3	8384	13	ADU38674	Adu38674	TipA	prom
	24	6306	77.0	8388	13	ADU38675	Adu38675	TipA	prom
	25	6215.6	75.9	8275	13	ADU38672	Adu38672	TipA	prom
	26	6188.8	75.6	8279	13	ADU38673	Adu38673	TipA	prom
	27	4827.2	58.9	5984	13	ADT49717	Adt49717	Cell-free	
	28	4827.2	58.9	5984	13	ADU38678	Adu38678	TipA	prom
	29	4800.4	58.6	5988	13	ADU38679	Adu38679	TipA	prom
	30	4393.8	53.7	8452	13	ADU38676	Adu38676	TipA	prom
	31	4367	53.3	8456	13	ADU38677	Adu38677	TipA	prom
	32	4341.4	53.0	6153	13	ADU38682	Adu38682	TipA	prom
	33	4314.6	52.7	6157	13	ADU38683	Adu38683	TipA	prom
	34	3519.2	43.0	5108	12	ADL71918	Adl71918	Nucleotid	
	35	2899.2	35.4	6058	13	ADU38680	Adu38680	TipA	prom
	36	2872.4	35.1	6062	13	ADU38681	Adu38681	TipA	prom
	37	2413.4	29.5	6227	13	ADU38684	Adu38684	TipA	prom
	38	2386.6	29.1	6231	13	ADU38685	Adu38685	TipA	prom
c	39	2063.2	25.2	8497	14	AEA02112	Aea02112	pRET1001R	
	40	2010.4	24.6	7327	15	AEH33678	Aeh33678	Plasmid	p
	41	2008.8	24.5	2946	3	AAA75650	Aaa75650	Nucleotid	
	42	2008.8	24.5	3723	4	AAD10000	Aad10000	Plasmid	p
	43	2008.8	24.5	4274	2	AAQ54144	Aaq54144	Sequence	
c	44	2008.8	24.5	4313	15	AEH65683	Aeh65683	Plasmid	p
c	45	2008.8	24.5	4313	15	AEH46471	Aeh46471	Plasmid	p

ALIGNMENTS

RESULT 1

ADL06264

ID ADL06264 standard; DNA; 8189 BP.

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AC ADL06264;

XX

DT 20-MAY-2004 (first entry)

XX

DE DNA sequence of vector pTipLNH1.

XX

KW Expression vector; foreign gene; host cell; protein synthesis;

KW glycoprotein; tumour cell; gene therapy; cytostatic; ds.

XX

OS Unidentified.

XX

PN WO2004016792-A1.

XX

PD 26-FEB-2004.

XX

PF 11-AUG-2003; 2003WO-JP010209.

XX

PR 12-AUG-2002; 2002JP-00235008.

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PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

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